

OIPE

RAW SEQUENCE LISTING

DATE: 02/08/2001

PATENT APPLICATION: US/09/771,045

TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT

Output Set: N:\CRF3\02082001\I771045.raw

Does Not Comply
Corrected Diskette Needed.

P. 6

```

4 <110> APPLICANT: Duvick, Jonathan P.
5   Gilliam, Jacob T.
6   Maddox, Joyce R.
8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
9   Polynucleotides and Related Polypeptides and Methods of Use
12 <130> FILE REFERENCE: 1134C
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/771,045
C--> 14 <141> CURRENT FILING DATE: 2001-01-26
14 <150> PRIOR APPLICATION NUMBER: US 60/092,936
15 <151> PRIOR FILING DATE: 1998-07-15
17 <150> PRIOR APPLICATION NUMBER: US 60/135,391
18 <151> PRIOR FILING DATE: 1999-05-21
20 <150> PRIOR APPLICATION NUMBER: US 09/352,159
21 <151> PRIOR FILING DATE: 1999-07-12
23 <150> PRIOR APPLICATION NUMBER: US 09/352,168
24 <151> PRIOR FILING DATE: 1999-07-12
26 <160> NUMBER OF SEQ ID NOS: 53
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 372
32 <212> TYPE: DNA
33 <213> ORGANISM: Exophiala spinifera
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (346)...(346)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41   gggcccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgtcgtagctt      60
42   gcttggaactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc      120
43   attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt      180
44   ggaggacgcc cgagaagcct tgttcgcgcc accacggcct gtcccatacg aagactatct      240
45   tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagagggtg      300
46   gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc      360
47   ggaacacggc gc
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 182
51 <212> TYPE: DNA
52 <213> ORGANISM: Exophiala spinifera
54 <400> SEQUENCE: 2
55   gaattttccg ccaatgcttg cttctcggcg ggaagagggtg gtgaaaatgt caaggtggga      60
56   tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc      120
57   gatcgtagtg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgagggtgc      180
58   ac
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 29
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence

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65 <220> FEATURE:
66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
69 <400> SEQUENCE: 3
70   tggtttcggt accgacaacc ttgtatccc                29
72 <210> SEQ ID NO: 4
73 <211> LENGTH: 28
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
80 <400> SEQUENCE: 4
81   gagttggtcc cagacagact tttgtcgt                28
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 1389
85 <212> TYPE: DNA
86 <213> ORGANISM: Exophiala spinifera
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (1)...(1386)
92 <400> SEQUENCE: 5
93   gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg                48
94   Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
95   1      5      10     15
97   gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt                96
98   Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
99   20     25     30
101  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt                144
102  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
103  35     40     45
105  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac                192
106  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
107  50     55     60
109  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag                240
110  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
111  65     70     75     80
113  ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac                288
114  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
115  85     90     95
117  ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag                336
118  Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
119  100    105    110
121  gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc                384
122  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
123  115    120    125
125  gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg                432
126  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
127  130    135    140
129  ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg                480
130  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu

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131	145	150	155	160	
133	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt				528
134	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly				
135		165	170	175	
137	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag				576
138	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
139		180	185	190	
141	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg				624
142	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly				
143		195	200	205	
145	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg				672
146	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met				
147		210	215	220	
149	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct				720
150	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala				
151		225	230	235	240
153	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc				768
154	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly				
155		245	250	255	
157	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg				816
158	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu				
159		260	265	270	
161	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca				864
162	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala				
163		275	280	285	
165	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta				912
166	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val				
167		290	295	300	
169	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa				960
170	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln				
171		305	310	315	320
173	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc				1008
174	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val				
175		325	330	335	
177	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg				1056
178	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg				
179		340	345	350	
181	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac				1104
182	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp				
183		355	360	365	
185	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg				1152
186	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro				
187		370	375	380	
189	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga				1200
190	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly				
191		385	390	395	400
193	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg				1248
194	Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser				
195		405	410	415	

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197 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
198 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
199          420          425          430
201 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
202 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
203          435          440          445
205 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca      1386
206 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
207          450          455          460
209 tag      1389
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 462
213 <212> TYPE: PRT
214 <213> ORGANISM: Exophiala spinifera
216 <400> SEQUENCE: 6
217 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
218 1 5 10 15
219 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
220 20 25 30
221 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
222 35 40 45
223 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
224 50 55 60
225 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
226 65 70 75 80
227 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
228 85 90 95
229 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
230 100 105 110
231 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
232 115 120 125
233 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
234 130 135 140
235 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
236 145 150 155 160
237 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
238 165 170 175
239 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
240 180 185 190
241 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
242 195 200 205
243 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
244 210 215 220
245 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
246 225 230 235 240
247 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
248 245 250 255
249 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
250 260 265 270

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```

251 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
252          275          280          285
253 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
254          290          295          300
255 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
256          305          310          315          320
257 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
258          325          330          335
259 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
260          340          345          350
261 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
262          355          360          365
263 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
264          370          375          380
265 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
266          385          390          395          400
267 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
268          405          410          415
269 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
270          420          425          430
271 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
272          435          440          445
273 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
274          450          455          460
276 <210> SEQ ID NO: 7
277 <211> LENGTH: 1442
278 <212> TYPE: DNA
279 <213> ORGANISM: Exophiala spinifera
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)...(646)
285 <221> NAME/KEY: intron
286 <222> LOCATION: (647)...(699)
288 <221> NAME/KEY: CDS
289 <222> LOCATION: (700)...(1439)
291 <400> SEQUENCE: 7
292 gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg      48
293 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
294 1          5          10          15
296 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
297 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
298          20          25          30
300 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
301 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
302          35          40          45
304 ccc gcc agg acg act atc aac gac ctc gcc gct gcg tgg atc aat gac      192
305 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
306          50          55          60
308 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag      240

```

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<210> 19
<211> 692
<212> PRT
<213> Unknown
<400> 19

see item 12 on Error Summary Sheet



The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FWI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/771,045

DATE: 02/08/2001

TIME: 12:14:09

Input Set : A:\1134CSEQLIST.TXT

Output Set: N:\CRF3\02082001\I771045.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:349 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
 L:1234 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1334 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1335 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1488 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2095 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2517 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2989 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:2989 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:3153 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3154 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3487 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:3487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:3810 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:3810 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:4186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
 L:4247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

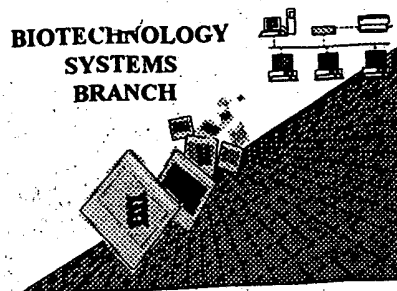
SERIAL NUMBER:

09/77,045

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/771,045
 Source: OIP
 Date Processed by STIC: 2/8/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>